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RAW SEQUENCE LISTING

DATE: 06/21/2002

PATENT APPLICATION: US/09/940,925A

TIME: 12:20:02

Input Set : A:\Seqsub2.app

Output Set: N:\CRF3\06212002\I940925A.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: BROW, MARY ANN D.
 7 LYAMICHEV, VICTOR I.
 8 OLIVE, DAVID M.

10 (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
 11 PATHOGENS

13 (iii) NUMBER OF SEQUENCES: 165

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: MEDLEN & CARROLL
 17 (B) STREET: 220 MONTGOMERY STREET, SUITE 2200
 18 (C) CITY: SAN FRANCISCO
 19 (D) STATE: CALIFORNIA
 20 (E) COUNTRY: UNITED STATES OF AMERICA
 21 (F) ZIP: 94104

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: IBM PC compatible
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/940,925A
 C--> 31 (B) FILING DATE: 10-Jun-2002
 32 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: CARROLL, PETER G.
 36 (B) REGISTRATION NUMBER: 32,837
 37 (C) REFERENCE/DOCKET NUMBER: FORS-01756

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (415) 705-8410
 41 (B) TELEFAX: (415) 397-8338

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 2506 base pairs
 48 (B) TYPE: nucleic acid
 49 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: DNA (genomic)

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58	ATGAGGGGGA TGCTGCCCCT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC	60
60	CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG	120
62	GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC	180
64	GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG	240

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66	TACAAGGCGG	GCCGGGCCCC	CACGCCGGAG	GACTTTCCCC	GGCAACTCGC	CCTCATCAAG	300
68	GAGCTGGTGG	ACCTCCTGGG	GCTGGCGCGC	CTCGAGGTCC	CGGGCTACGA	GGCGGACGAC	360
70	GTCCTGGCCA	GCCTGGCCAA	GAAGGCGGAA	AAGGAGGGCT	ACGAGGTCCG	CATCCTCACC	420
72	GCCGACAAAG	ACCTTTACCA	GCTCCTTTCC	GACCGCATCC	ACGTCCTCCA	CCCCGAGGGG	480
74	TACCTCATCA	CCCCGGCCTG	GCTTTGGGAA	AAGTACGGCC	TGAGGCCCGA	CCAGTGGGCC	540
76	GACTACCGGG	CCCTGACCGG	GGACGAGTCC	GACAACCTTC	CCGGGGTCAA	GGGCATCGGG	600
78	GAGAAGACGG	CGAGGAAGCT	TCTGGAGGAG	TGGGGGAGCC	TGGAAGCCCT	CCTCAAGAAC	660
80	CTGGACCGGC	TGAAGCCCGC	CATCCGGGAG	AAGATCCTGG	CCCACATGGA	CGATCTGAAG	720
82	CTCTCCTGGG	ACCTGGCCAA	GGTGCGCACC	GACCTGCCCC	TGGAGGTGGA	CTTCGCCAAA	780
84	AGGCGGGAGC	CCGACCGGGA	GAGGCTTAGG	GCCTTTCTGG	AGAGGCTTGA	GTTTGGCAGC	840
86	CTCCTCCACG	AGTTCGGCCT	TCTGGAAAGC	CCCAAGGCC	TGGAGGAGGC	CCCCTGGCCC	900
88	CCGCCGGAAG	GGGCCTTCGT	GGGCTTTGTG	CTTTCCCGCA	AGGAGCCCAT	GTGGGCCGAT	960
90	CTTCTGGCCC	TGGCCGCCGC	CAGGGGGGGC	CGGGTCCACC	GGGCCCCCGA	GCCTTATAAA	1020
92	GCCCTCAGGG	ACCTGAAGGA	GGCGCGGGGG	CTTCTCGCCA	AAGACCTGAG	CGTTCTGGCC	1080
94	CTGAGGGAAG	GCCTTGGCCT	CCCGCCCGGC	GACGACCCCA	TGCTCCTCGC	CTACCTCCTG	1140
96	GACCCTTCCA	ACACCACCCC	CGAGGGGGTG	GCCCGGCGCT	ACGGCGGGGA	GTGGACGGAG	1200
98	GAGGCGGGGG	AGCGGGCCGC	CCTTTCCGAG	AGGCTCTTCG	CCAACCTGTG	GGGGAGGCTT	1260
100	GAGGGGGAGG	AGAGGCTCCT	TTGGCTTTAC	CGGGAGGTGG	AGAGGCCCTT	TTCCGCTGTC	1320
102	CTGGCCCACA	TGGAGGCCAC	GGGGGTGCGC	CTGGACGTGG	CCTATCTCAG	GGCCTTGTC	1380
104	CTGGAGGTGG	CCGAGGAGAT	CGCCCGCCTC	GAGGCCGAGG	TCTTCCGCCT	GGCCGGCCAC	1440
106	CCCTTCAACC	TCAACTCCCG	GGACCAGCTG	GAAAGGGTCC	TCTTTGACGA	GCTAGGGCTT	1500
108	CCCGCCATCG	GCAAGACGGA	GAAGACCGGC	AAGCGCTCCA	CCAGCGCCGC	CGTCCTGGAG	1560
110	GCCCTCCGCG	AGGCCACCCC	CATCGTGGAG	AAGATCCTGC	AGTACCGGGA	GCTCACCAAG	1620
112	CTGAAGAGCA	CCTACATTGA	CCCCTTGCCG	GACCTCATCC	ACCCAGGAC	GGGCCGCCTC	1680
114	CACACCCGCT	TCAACCAGAC	GGCCACGGCC	ACGGGCAGGC	TAAGTAGCTC	CGATCCCAAC	1740
116	CTCCAGAACA	TCCCCGTCCG	CACCCCGCTT	GGGCAGAGGA	TCCGCCGGGC	CTTCATCGCC	1800
118	GAGGAGGGGT	GGCTATTGGT	GGCCCTGGAC	TATAGCCAGA	TAGAGCTCAG	GGTGCTGGCC	1860
120	CACCTCTCCG	GCGACGAGAA	CCTGATCCGG	GTCTTCCAGG	AGGGGCGGGA	CATCCACACG	1920
122	GAGACCGCCA	GCTGGATGTT	CGGCGTCCCC	CGGGAGGCCG	TGGACCCCTT	GATGCGCCGG	1980
124	GCGGCCAAGA	CCATCAACTT	CGGGGTCCCTC	TACGGCATGT	CGGCCACCG	CCTCTCCCAG	2040
126	GAGCTAGCCA	TCCCTTACGA	GGAGGCCAG	GCCTTCATTG	AGCGCTACTT	TCAGAGCTTC	2100
128	CCCAAGGTGC	GGGCCTGGAT	TGAGAAGACC	CTGGAGGAGG	GCAGGAGGCG	GGGGTACGTG	2160
130	GAGACCCTCT	TCGGCCGCCG	CCGCTACGTG	CCAGACCTAG	AGGCCCGGGT	GAAGAGCGTG	2220
132	CGGGAGGCGG	CCGAGCGCAT	GGCCTTCAAC	ATGCCCCTCC	AGGGCACCGC	CGCCGACCTC	2280
134	ATGAAGCTGG	CTATGGTGAA	GCTCTTCCCC	AGGCTGGAGG	AAATGGGGGC	CAGGATGCTC	2340
136	CTTCAGGTCC	ACGACGAGCT	GGTCCTCGAG	GCCCCAAAAG	AGAGGGCGGA	GGCCGTGGCC	2400
138	CGGCTGGCCA	AGGAGGTCAT	GGAGGGGGTG	TATCCCCTGG	CCGTGCCCCT	GGAGGTGGAG	2460
140	GTGGGGATAG	GGGAGGACTG	GCTCTCCGCC	AAGGAGTGAT	ACCACC		2506

142 (2) INFORMATION FOR SEQ ID NO: 2:

144 (i) SEQUENCE CHARACTERISTICS:

145 (A) LENGTH: 2496 base pairs

146 (B) TYPE: nucleic acid

147 (C) STRANDEDNESS: double

148 (D) TOPOLOGY: linear

150 (ii) MOLECULE TYPE: DNA (genomic)

154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

156	ATGGCGATGC	TTCCCCTCTT	TGAGCCCAAA	GGCCGCGTGC	TCCTGGTGGG	CGGCCACCAC	60
158	CTGGCCTACC	GCACCTTCTT	TGCCCTCAAG	GGCCTCACCA	CCAGCCGCGG	CGAACCCGTT	120
160	CAGGCGGTCT	ACGGCTTCGC	CAAAAGCCTC	CTCAAGGCC	TGAAGGAGGA	CGGGGACGTG	180

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162	GTGGTGGTGG	TCTTTGACGC	CAAGGCCCCC	TCCTTCCGCC	ACGAGGCCTA	CGAGGCCTAC	240
164	AAGGCGGGCC	GGGCCCCC	CCCGGAGGAC	TTTCCCCGGC	AGCTGGCCCT	CATCAAGGAG	300
166	TTGGTGGACC	TCCTAGGCCT	TGTGCGGCTG	GAGGTTCCTG	GCTTTGAGGC	GGACGACGTG	360
168	CTGGCCACCC	TGGCCAAGCG	GGCGGAAAAG	GAGGGGTACG	AGGTGCGCAT	CCTCACTGCC	420
170	GACCGCGACC	TCTACCAGCT	CCTTTCGGAG	CGCATCGCCA	TCCTCCACCC	TGAGGGGTAC	480
172	CTGATCACCC	CGGCGTGGCT	TTACGAGAAG	TACGGCCTGC	GCCCGGAGCA	GTGGGTGGAC	540
174	TACCGGGCCC	TGGCGGGGGA	CCCCTCGGAT	AACATCCCCG	GGGTGAAGGG	CATCGGGGAG	600
176	AAGACCGCCC	AGAGGCTCAT	CCGCGAGTGG	GGGAGCCTGG	AAAACCTCTT	CCAGCACCTG	660
178	GACCAGGTGA	AGCCCTCCTT	GCGGGAGAAG	CTCCAGGCGG	GCATGGAGGC	CCTGGCCCTT	720
180	TCCCGGAAGC	TTTCCCAGGT	GCACACTGAC	CTGCCCTTGG	AGGTGGACTT	CGGGAGGCGC	780
182	CGCACACCCA	ACCTGGAGGG	TCTGCGGGCT	TTTTTTGGAGC	GGTTGGAGTT	TGGAAGCCTC	840
184	CTCCACGAGT	TCGGCCTCCT	GGAGGGGCGG	AAGGCGGCAG	AGGAGGCCCC	CTGGCCCCCT	900
186	CCGGAAGGGG	CTTTTTTTGGG	CTTTTCCTTT	TCCCGTCCCC	AGCCCATGTG	GGCCGAGCTT	960
188	CTGGCCCTGG	CTGGGGCGTG	GGAGGGGCGC	CTCCATCGGG	CACAAGACCC	CCTTAGGGGC	1020
190	CTGAGGGACC	TTAAGGGGGT	GCGGGGAATC	CTGGCCAAGG	ACCTGGCGGT	TTTGGCCCTG	1080
192	CGGGAGGGCC	TGGACCTCTT	CCCAGAGGAC	GACCCCATGC	TCCTGGCCTA	CCTTCTGGAC	1140
194	CCCTCCAACA	CCACCCCTGA	GGGGGTGGCC	CGGCGTTACG	GGGGGGAGTG	GACGGAGGAT	1200
196	GCGGGGGAGA	GGGCCCTCCT	GGCCGAGCGC	CTCTTCCAGA	CCCTAAAGGA	GCGCCTTAAG	1260
198	GGAGAAGAAC	GCCTGCTTTG	GCTTTACGAG	GAGGTGGAGA	AGCCGCTTTC	CCGGGTGTTG	1320
200	GCCCGGATGG	AGGCCACGGG	GGTCCGGCTG	GACGTGGCCT	ACCTCCAGGC	CCTCTCCCTG	1380
202	GAGGTGGAGG	CGGAGGTGCG	CCAGCTGGAG	GAGGAGGTCT	TCCGCCTGGC	CGGCCACCCC	1440
204	TTCAACCTCA	ACTCCCGCGA	CCAGCTGGAG	CGGGTGCTCT	TTGACGAGCT	GGGCCTGCCT	1500
206	GCCATCGGCA	AGACGGAGAA	GACGGGGAAA	CGCTCCACCA	GCGCTGCCGT	GCTGGAGGCC	1560
208	CTGCGAGAGG	CCCACCCCAT	CGTGGACCGC	ATCCTGCAGT	ACCGGGAGCT	CACCAAGCTC	1620
210	AAGAACACCT	ACATAGACCC	CCTGCCCCGC	CTGGTCCACC	CCAAGACCGG	CCGGCTCCAC	1680
212	ACCCGCTTCA	ACCAGACGGC	CACCGCCACG	GGCAGGCTTT	CCAGCTCCGA	CCCCAACCTG	1740
214	CAGAACATCC	CCGTGCGCAC	CCCTCTGGGC	CAGCGCATCC	GCCGAGCCTT	CGTGGCCGAG	1800
216	GAGGGCTGGG	TGCTGGTGGT	CTTGGACTAC	AGCCAGATTG	AGCTTCGGGT	CCTGGCCCAC	1860
218	CTCTCCGGGG	ACGAGAACCT	GATCCGGGTC	TTTCAGGAGG	GGAGGGACAT	CCACACCCAG	1920
220	ACCGCCAGCT	GGATGTTTCG	CGTTTCCCCC	GAAGGGGTAG	ACCCTCTGAT	GCGCCGGGCG	1980
222	GCCAAGACCA	TCAACTTCGG	GGTGCTCTAC	GGCATGTCCG	CCCACCGCCT	CTCCGGGGAG	2040
224	CTTTCCATCC	CCTACGAGGA	GGCGGTGGCC	TTCATTGAGC	GCTACTTCCA	GAGCTACCCC	2100
226	AAGGTGCGGG	CCTGGATTGA	GGGGACCCTC	GAGGAGGGCC	GCCGGCGGGG	GTATGTGGAG	2160
228	ACCCTCTTCG	GCCGCCGGCG	CTATGTGCCC	GACCTCAACG	CCCGGGTGAA	GAGCGTGCGC	2220
230	GAGGCGGCGG	AGCGCATGGC	CTTCAACATG	CCGGTCCAGG	GCACCGCCGC	CGACCTCATG	2280
232	AAGCTGGCCA	TGGTGCGGCT	TTTCCCCCGG	CTTCAGGAAC	TGGGGGCGAG	GATGCTTTTG	2340
234	CAGGTGCACG	ACGAGCTGGT	CCTCGAGGCC	CCCAAGGACC	GGGCGGAGAG	GGTAGCCGCT	2400
236	TTGGCCAAGG	AGGTCATGGA	GGGGGTCTGG	CCCCTGCAGG	TGCCCCCTGA	GGTGGAGGTG	2460
238	GGCCTGGGGG	AGGACTGGCT	CTCCGCCAAG	GAGTAG			2496
240	(2) INFORMATION FOR SEQ ID NO: 3:						
242	(i) SEQUENCE CHARACTERISTICS:						
243	(A) LENGTH: 2504 base pairs						
244	(B) TYPE: nucleic acid						
245	(C) STRANDEDNESS: double						
246	(D) TOPOLOGY: linear						
248	(ii) MOLECULE TYPE: DNA (genomic)						
252	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:						
254	ATGGAGGCGA	TGCTTCCGCT	CTTTGAACCC	AAAGGCCGGG	TCCTCCTGGT	GGACGGCCAC	60
256	CACCTGGCCT	ACCGCACCTT	CTTCGCCCTG	AAGGGCCTCA	CCACGAGCCG	GGGCGAACCG	120

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258 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC 180
260 AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCTCCT TCCGCCACGA GGCCTACGAG 240
262 GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC 300
264 AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC 360
266 GACGTTCTCG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC 420
268 ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCCGAG 480
270 GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG 540
272 GTGGAATTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC 600
274 GGGGAGAAGA CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG 660
276 AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCCA CCTGGAAGAC 720
278 CTCAGGCTCT CCTTGAGCT CTCCCGGGTG CGCACCGACC TCCCCCTGGA GGTGGACCTC 780
280 GCCCAGGGGC GGGAGCCCGA CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC 840
282 GGCAGCCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCCTGGA GGAGGCCCCC 900
284 TGGCCCCCGC CGGAAGGGGC CTTCGTGGGC TTCGTCCTCT CCCGCCCGA GCCCATGTGG 960
286 GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC 1020
288 TTGGCGGGGC TAAAGGACCT CAAGGAGGTC CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC 1080
290 TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCATGCT CCTCGCCTAC 1140
292 CTCCTGGACC CCTCCAACAC CACCCCGAG GGGGTGGCGC GGCCTACGG GGGGGAGTGG 1200
294 ACGGAGGACG CCGCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG 1260
296 CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCACG AGGTGGAAAA GCCCCTCTCC 1320
298 CGGGTCCTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CCTTCAGGCC 1380
300 CTTTCCCTGG AGCTTGCGGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG 1440
302 GGCCACCCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT 1500
304 AGGCTTCCCG CCTTGGGGAA GACGCAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG 1560
306 CTGGAGGCC TACGGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC 1620
308 ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCAAGCC TCGTCCACCC GAGGACGGGC 1680
310 CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC 1740
312 CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC 1800
314 GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC 1860
316 CTCGCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC 1920
318 CACACCCAGA CCGCAAGCTG GATGTTCGGC GTCCCCCGG AGGCCGTGGA CCCCTGATG 1980
320 CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC 2040
322 TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA 2100
324 GCTTCCCAA GGTGCGGGCC TGGATAGAAA AGACCTGGA GGAGGGGAGG AAGCGGGGCT 2160
326 ACGTGGAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA 2220
328 GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCG 2280
330 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCGCCT CCGGGAGATG GGGGCCCGCA 2340
332 TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAG 2400
334 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG 2460
336 TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG 2504

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338 (2) INFORMATION FOR SEQ ID NO: 4:

340 (i) SEQUENCE CHARACTERISTICS:

341 (A) LENGTH: 832 amino acids

342 (B) TYPE: amino acid

343 (C) STRANDEDNESS: single

344 (D) TOPOLOGY: linear

346 (ii) MOLECULE TYPE: protein

350 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

352 Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu

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353	1	5	10	15
355	Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly			
356		20	25	30
358	Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala			
359		35	40	45
361	Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val			
362		50	55	60
364	Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly			
365	65		70	75
367	Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu			
368		85	90	95
370	Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu			
371		100	105	110
373	Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys			
374		115	120	125
376	Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp			
377		130	135	140
379	Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly			
380	145		150	155
382	Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro			
383		165	170	175
385	Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn			
386		180	185	190
388	Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu			
389		195	200	205
391	Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu			
392		210	215	220
394	Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys			
395	225		230	235
397	Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val			
398		245	250	255
400	Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe			
401		260	265	270
403	Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu			
404		275	280	285
406	Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly			
407		290	295	300
409	Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp			
410	305		310	315
412	Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro			
413		325	330	335
415	Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu			
416		340	345	350
418	Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro			
419		355	360	365
421	Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn			
422		370	375	380
424	Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu			
425	385		390	395